

RESULT 1
 AK045869
 LOCUS AK045869 4642 bp mRNA linear HTC 02-SEP-2005
 DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN
 full-length enriched library, clone:B230315M08 product:MMAC8
 precursor (MAIR-Ib), full insert sequence.
 ACCESSION AK045869
 VERSION AK045869.1 GI:26337658
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
 Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
 Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
 and Hayashizaki, Y.
 CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 PUBMED 11217851

REFERENCE 5

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaïdo, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawaji, H., Kawasaki, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
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 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

CONSRM FANTOM Consortium; RIKEN Genome Exploration Research Group Phase I
 & II Team

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED 12466851

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AUTHORS

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C.,
 Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R.,
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 Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E.,
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 Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,
 Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R.,
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 Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L.,
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Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,
Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,
Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,
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Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M.,
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Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
Watahiki,A., Okamura-Oho,Y., Suzuki,H.; Kawai,J. and Hayashizaki,Y.

CONSRTM FANTOM Consortium; RIKEN Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group)

TITLE The transcriptional landscape of the mammalian genome

JOURNAL Science 309 (5740), 1559-1563 (2005)

PUBMED 16141072

REFERENCE 7

AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
Wahlestedt,C.

CONSRTM RIKEN Genome Exploration Research Group; Genome Science Group
(Genome Network Project Core Group); FANTOM Consortium

TITLE Antisense transcription in the mammalian transcriptome

JOURNAL Science 309 (5740), 1564-1566 (2005)

PUBMED 16141073

REFERENCE 8 (bases 1 to 4642)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES
source Location/Qualifiers
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